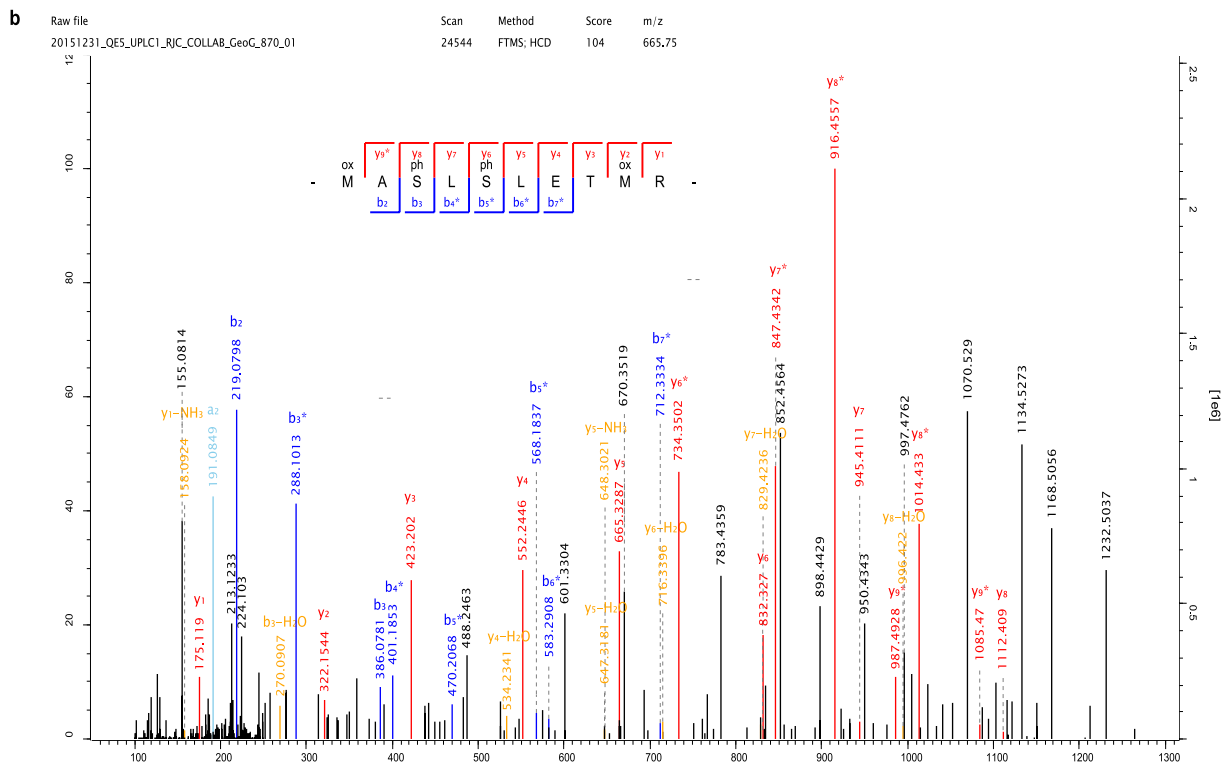
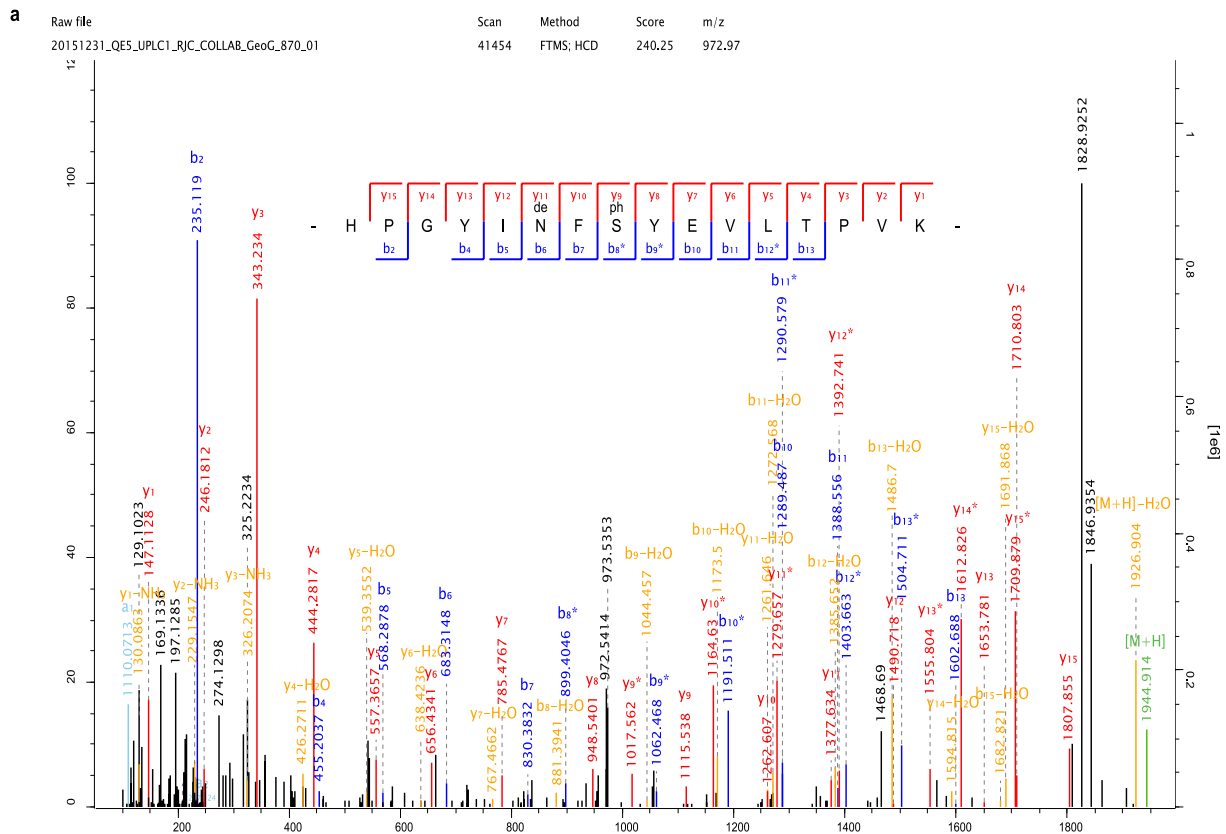


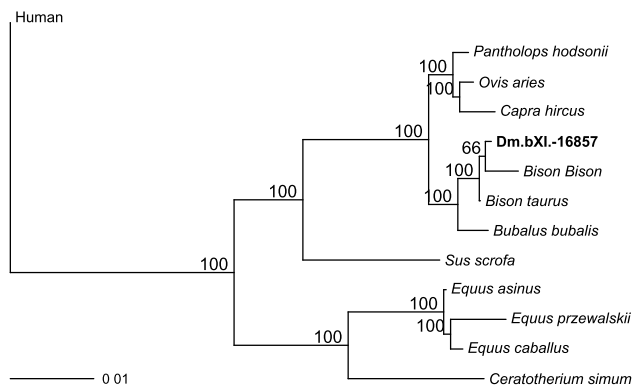
Extended Data Fig. 4 | Amino acid racemization. Extent of intra-crystalline racemization in enamel for the free amino acid (FAA, x axis) fraction and the total hydrolysable amino acids (THAA, y axis) fraction for four amino acids (Asp plus Asn (here denoted Asx), Glu plus Gln (here denoted Glx), Ala and Phe). Note the differences in axis scale.

Intra-crystalline data from Proboscidea enamel from a range of sites in the UK⁶⁴ have been shown for comparison (grey crosses). Taxa from both Dmanisi and the UK exhibit a similar relationship between FAA and THAA racemization, and R^2 values have been calculated on the basis of a polynomial relationship (order = 2, all > 0.93).

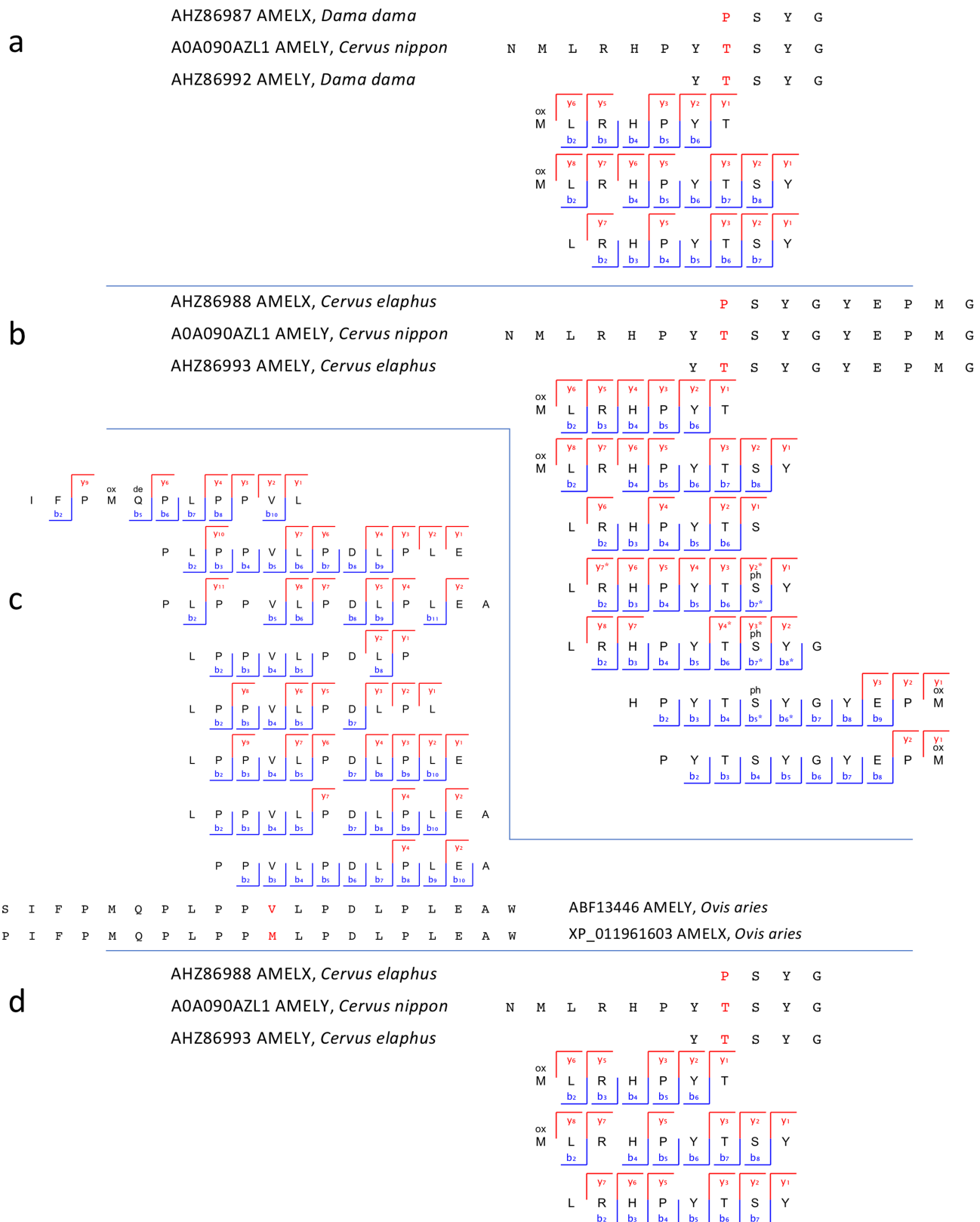


Extended Data Fig. 5 | Phosphorylation in the proteome of ancient enamel. Annotated spectra including phosphorylated (here denoted ph) serine (S). **a**, Phosphorylation in the S-X-E motif of AMELX. **b**, Phosphorylation in the S-X-phosphorylated S motif of AMBN.

Phosphorylation was independently observed in all three separate analyses of Dm.5/157–16635, including multiple spectra and peptides (Extended Data Fig. 2).

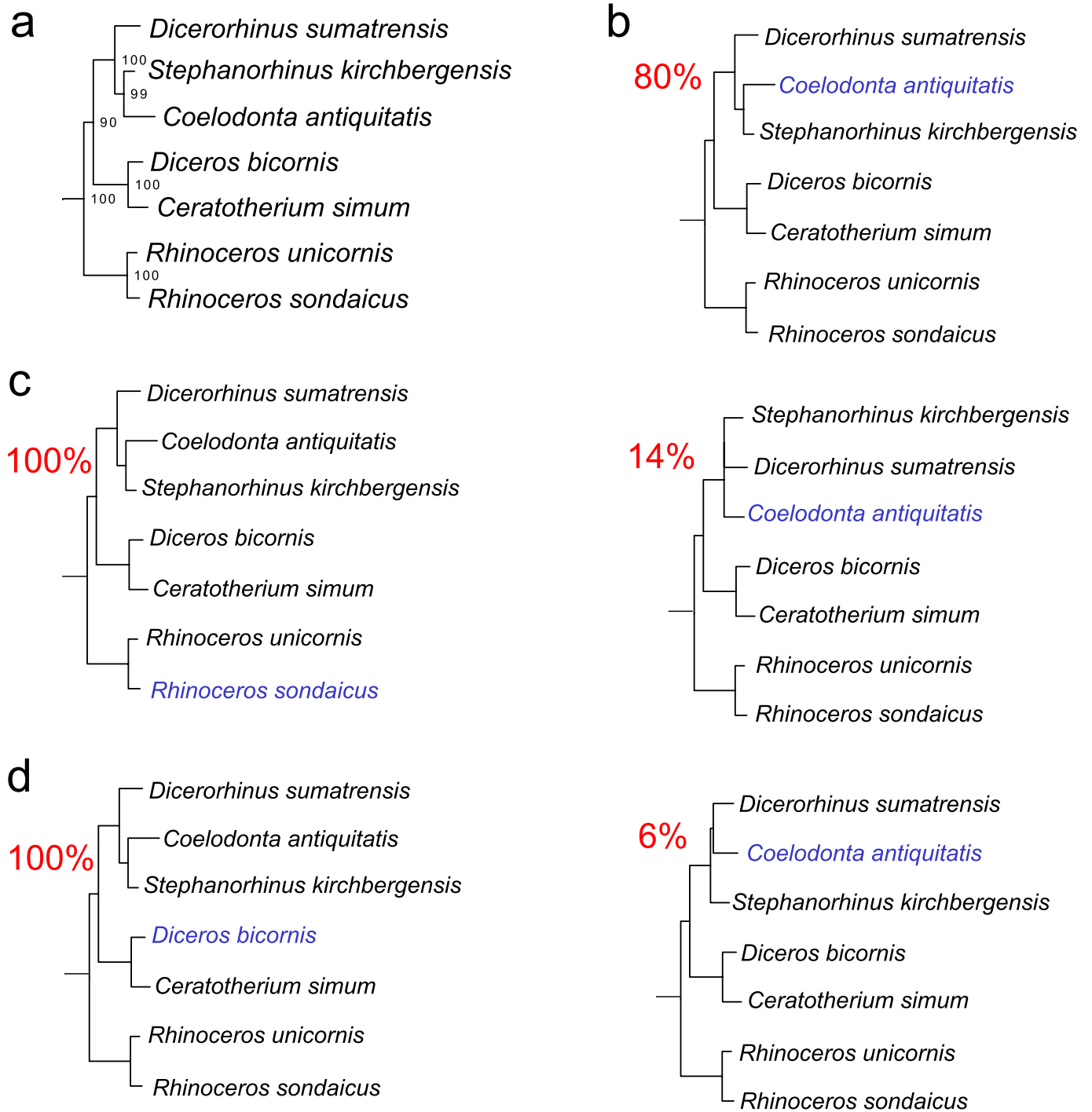


Extended Data Fig. 6 | Phylogenetic relationships between the comparative reference dataset and specimen Dm.bXI-16857. Consensus tree from Bayesian inference. The posterior probability of each bipartition is shown as a percentage to the left of each node.



Extended Data Fig. 7 | AMELY-specific matches. a, Specimen Dm.6/151.4.A4.12–16630. b, Specimen Dm.69/64.3.B1.53–16631. c, Specimen Dm.8/154.4.A4.22–16639. d, Specimen Dm.M6/7.II.296–

16856. Note the presence of deamidated glutamine (deQ) and asparagine (deN), oxidated methionine (oxM) and phosphorylated serine (phS).



Extended Data Fig. 8 | Effect of the missingness in the tree topology. **a**, Maximum-likelihood phylogeny obtained using PhyML and the protein alignment that excludes Dm.5/157–16635. **b**, Topologies obtained from 100 random replicates of the woolly rhinoceros (*C. antiquitatis*). In each replicate, the number of missing sites was similar to that observed for

the Dm.5/157–16635 specimen (72.4% missingness). The percentage shown for each topology indicates the number of replicates in which that particular topology was recovered. **c**, As in **b**, but for the Javan rhinoceros (*R. sondaicus*). **d**, As in **b**, but for the black rhinoceros (*D. bicornis*).

Extended Data Table 1 | Genome and proteome survival in 23 specimens of fossil fauna from Dmanisi

CGG ref. numb.	GNM specimen number	Morphological identification*	Anatomy	Ancient DNA	Protein extr. Method A	Protein extr. Method B	Protein extr. Method C	Phylogenetic analysis
16486	Dm.bXI.sqA6.V.1.	<i>Canis etruscus</i>	P4 sin.				○E+D	
16626	Dm.6/154.2/4.A4.17	Artiodactyla	tibia sin.			○B		
16628	Dm.7/154.2.A2.27	Cervidae	mc III&IV dex.			●B†		
16629	Dm.5/154.3.A4.32	Cervidae	hemimandible sin. with dp2, dp3, dp4, m1			○B	●E+D	
16630	Dm.6/151.4.A4.12	<i>Pseudodama nestii</i>	hemimandible dex. with p2-m3			○B	○D, ●E	
16631	Dm.69/64.3.B1.53	Cervidae	maxilla sin. with P3			○B	○D, ●E	
16632	Dm.5/154.2.A4.38	<i>Equus stenonis</i>	i3 dex.				●E+D	Fig. S10
16633	Dm.5/153.3.A2.33	<i>Equus stenonis</i>	mc III & mc II sin.				○B	
16634	Dm.7/151.2.B1/A4.1	<i>Equus stenonis</i>	m/1 or m/2 dex.				○D, ●E	
16635	Dm.5/157.profile cleaning	<i>Stephanorhinus</i> sp.	m/1 sin.	○			○D, ●E	Fig. 4, Fig. S11
16636	Dm.6/153.1.A4.13	Rhinocerotidae	tibia dex.			○B		
16637	Dm.7/154.2.A4.8	Bovidae	mt III&IV sin.			●B†		
16638	Dm.5/154.1.B1.1	Bovidae	hemimandible dex. with p3-m3			○B	○D, ●E	Fig. S12
16639	Dm.8/154.4.A4.22	Bovidae	maxilla dex. with P2-M2				○D, ●E	Fig. S13
16640	Dm.6/151.2.A4.97	<i>Bison georgicus</i>	mt III&IV sin.			○B		
16641	Dm.8/152.3.B1.2	<i>Bison georgicus</i>	m3 dex.				○D, ●E	Fig. S14
16642	Dm.8/153.4.A4.5	<i>Canis etruscus</i>	hemimandible sin. with p1-m2				○D, ●E	
16856	Dm.M6/7.II.296	Cervidae	m2 sin.	○	●D†	○D, ●E	●E+D	
16857	Dm.bXI.profile cleaning	Indet.	long bone fragment of a herbivore	○	●B†	○B	○B	Fig. S15, EDF6
16858	Dm.bXI.North.B1a.collection	Cervidae	metapodium fragment		○B	○B	○B	
16859	D4.collection	Indet.	fragments of pelvis and ribs of a large mammal	○	○B	○B	○B	
16860	Dm.65/62.1.A1.collection	Cervidae	P4 sin.	○		○D, ●E	○D, ●E	
16861	Dm.64/63.1.B1z.collection	<i>Equus stenonis</i>	fragment of an upper tooth			○D, ●E	○D, ●E	
Neg. contr. (blank)					NC	NC	NC	

The CGG reference number and the GNM specimen field number are reported for each specimen. B, bone; D, dentine; E, enamel. Extractions of enamel might include some residual dentine. Accordingly, both tissues are either listed separately (in cases with no collagen preservation) or together (in cases with collagen preservation). Open circles indicate no molecular preservation; closed circles indicate molecular preservation.

*Or the narrowest possible taxonomic identification achievable using comparative anatomy methods.
†Only collagens survive.